AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

Claim 1 (original): A method for detecting viral protein-protein interactions, said method comprising the steps of:

a) constructing a library of randomly-generated genomic viral DNA fragments in a DNA-binding domain vector,

b) constructing a library of randomly-generated genomic viral DNA fragments in an activation domain vector; and

c) assaying the library in the DNA-binding domain vector with the library in the activation domain vector by two-hybrid screening.

Claim 2 (original): The method of claim 1, wherein either or both of said libraries is prepared from the hepatitis C virus genome or from the hepatitis G virus genome.

Claim 3 (original): The method of claim 1, wherein either or both of said libraries is prepared from a cloned viral genome that is from a virus selected from the group consisting of herpes virus, potyvirus, flavivirus, and pestivirus.

Claim 4 (original): The method of claim 1, wherein either or both of said libraries is prepared from a cloned viral genome that encodes a polyprotein precursor.

Claim 5 (cancelled).

Claim 6 (original): A method for detecting viral protein-protein interactions, said method comprising the steps of:

a) constructing a library of DNA fragments in a DNA binding domain vector, wherein at least one DNA fragment encodes at least one molecule that interacts with viral proteins, and wherein said at least one molecule is selected from the group consisting of protein, polypeptide, and peptide;

b) constructing a library of DNA fragments in an activation domain vector, wherein at least one DNA fragment encodes at least one molecule that interacts with viral proteins, and wherein said at least one molecule is selected from the group consisting of protein, polypeptide, and peptide; and

c) assaying the library in the DNA-binding vector with the library in the activation domain vector by two-hybrid screening.

Claim 7 (original): The method of claim 6, wherein said protein is selected from the group consisting of an antibody, a receptor, a DNA binding protein, a glycoprotein, and a lipoprotein.

Claim 8 (original): The method according to claim 1, wherein at least one peptide is expressed from the library in the DNA-binding vector and wherein the peptide is a variant molecule compared to the known wild type viral peptide.

Claim 9 (original): The method according to claim 8, wherein the variant peptide presents at least one mutation selected from the group consisting of deletion, substitution, and insertion of at least one amino acid residue.

Claims 10-21 (cancelled).

Claim 22 (new): The method of claim 1, wherein the library of randomly-generated genomic viral DNA fragments in an activation domain vector is the GRBHCVL1 library deposited with the C.N.C.M. under accession number 1-2039 on June 15, 1998.

Claim 23 (new): The method of claim 1, wherein the library of randomly-generated genomic viral DNA fragments in a DNA-binding domain vector is the GRBHCVL2 library deposited with the C.N.C.M. under the accession number 1-2040 on June 15, 1998.

Claim 24 (new): The method of claim 1, wherein the library of randomly-generated genomic viral DNA fragments in an activation domain vector is the GRBHCVL1 library deposited with the C.N.C.M. under accession number 1-2039 on June 15, 1998; and wherein the library of randomly-generated genomic viral DNA fragments in a DNA-binding domain vector is the GRBHCVL2 library deposited with the C.N.C.M. under the accession number 1-2040 on June 15, 1998.